

Amphitrite Cross Selection Web Application	2
Backups	3
Fish Page	4
Recommend Crosses Workflow	8
Completed Crosses Page	12
User Management	15
User Settings	16
Running Software	17
Data Model Diagram	18
Cross Selection Algorithm	22

Amphitrite Cross Selection Web Application

Running the Software

[Running Software](#)

Using the Software

[Fish Page](#)

[Recommend Crosses Workflow](#)

[Completed Crosses Page](#)

[User Management](#)

[User Settings](#)

Data Model

[Data Model Diagram](#)

Cross Selection Algorithm

[Cross Selection Algorithm](#)

Managing the Software

[Backups](#)

Backups

Creation Policy

Snapshots of the volume the EC2 instance the application is running on are performed everyday. The snapshots are retained 7 days before being deleted.

Restore

In order to restore from a volume snapshot go the EC2 dashboard:

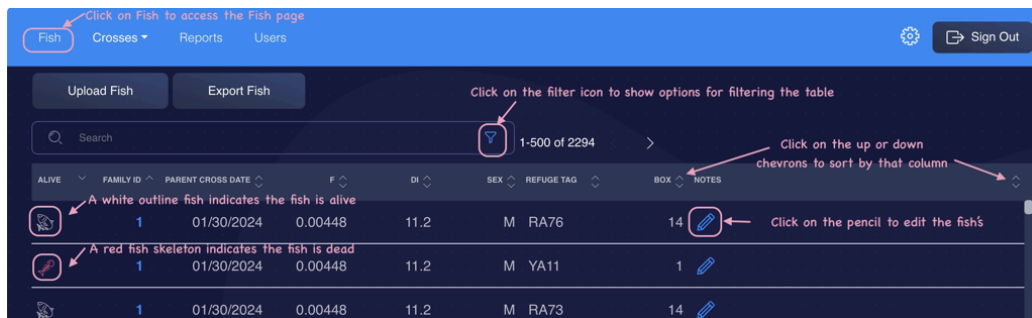
1. Select “Elastic Block Store”→Snapshots
2. Select the snapshot to restore from (most likely the latest)
3. Under Actions dropdown menu, select “Create Image from snapshot”
4. Give the image a name
5. Select Arm64 for architecture
6. Click “Create Image”
7. Go to Images→AMIs, Look for newly created image in list. You may have to hit the refresh button above the list in order for your new image to appear.
8. Select your new AMI
9. Click on “Launch Instance From AMI”
10. Name the server (e.g. Amphi Backup)
11. Select Instance type of t4g.medium
12. Under “Key pair (login)” select: amphitrite2.pem
13. Under “Common Security Groups” select: launch-wizard-2 sg-00287e918edd49912
14. Click “Launch Instance”
15. Once the instance is launched, find the Public IPv4 DNS in the Instance Summary for the new instance.
16. Connect to the new ECS instance:

```
>ssh -i ~/.ssh/amphitrite2.pem.pem ec2-user@<public IPV4 DNS name>
```
17. On the EC2 instance start the docker project:

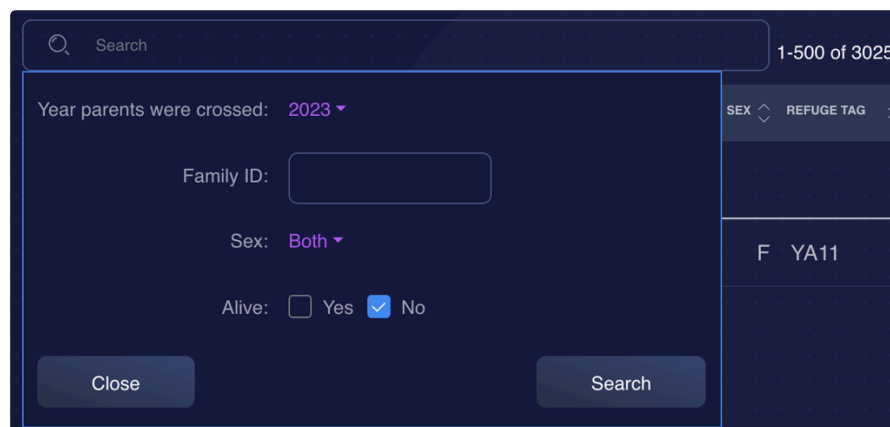
```
[ec2-user@<EC2 instance IP> ~]$ docker compose -f compose.yaml -p amphi up -d
```

Fish Page

Shows table with all the known fish as shown in the figure below:



When the page first loads, a default filter is set so that only *alive* fish whose parents were crossed in the previous year are included. To include other fish, click on the filter and adjust as necessary. The filter options are shown below.

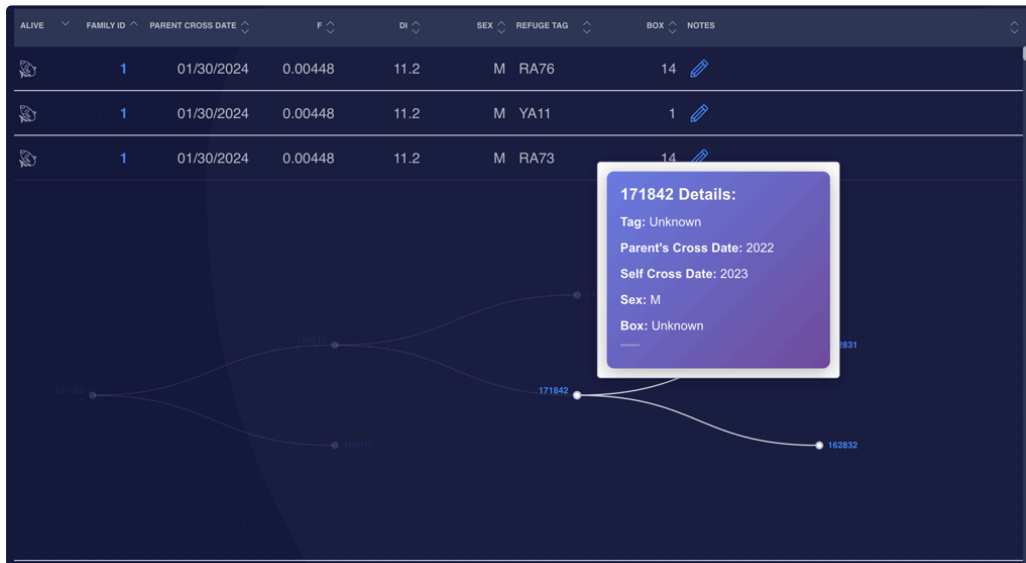


To include both dead and alive fish, check both the “Yes” and “No” boxes. To include only dead fish, select “No” and to select only alive fish, select “Yes”.

To filter the table, by other values, then those included in the Filter dialog, the “Search” bar above the table can be used. For example, it is possible to search for ‘YA’, which would result in a table, including all fish that pass the current filter and have tags beginning with ‘YA’.

Pedigree

The ancestry of any given fish can also be viewed in the Fish Table. In order to open the pedigree view for a fish, click on the Family Id. See image below:



In order to see information about a specific ancestor, mouse over that ancestor node. In order to see ancestors of an ancestor, click on the node and the pedigree graph will open an additional generation. To close an opened generation, click on the node again. The number displayed next to a node, is the generation ID of that fish.

Importing

In order to include new fish that the refuge has tagged, a master fish file that is a csv (i.e. values/columns are separated by commas) can be loaded. The file must contain the following columns in this order:

Notes,Tag,Sex,Family Id,Box,Allele Value 1,...,Allele Value 150

The ID Column is refuge tag, in the following formation: **RA73_2** where the _ and 1 or 2 following the underscore are ignored. If the fish is a 2 year old, a '2' should be prepended to the tag, i.e. in this case: 2RA73_2.

While the file is uploading, a spinner will show on the page. If the spinner fails to disappear after a few minutes, the page can be reloaded to see if the new fish have been uploaded. It is important not to begin selecting crosses until the import has complete. Once the “available fish” have been set in the “Request Crosses” page, newly imported fish will not be included in possible crosses.

Importing Updates

If a fish has had changes to its data and those changes are included in a new import, the fish will be updated to reflect the changes. In order to determine if a fish is the same as a fish that already exists in the software, the allele values of the fish are used to make matches. For

example, if a fish that is included in the import has allele values that all match a fish in the software, but their tags differ, the tag of the fish in the database will be updated to match the tag of the fish in the imported file.

Changes to Allele Values

Because the allele values are used to match fish, if changes need to be made to an existing fish's allele values, this *cannot* be done through the import feature. If the allele values are changed in the spreadsheet, no match will be found and an *additional* fish will be created. This will manifest as 2 fish with the same refuge tag (assuming the refuge tag also did not change). In order to change the allele values for existing fish, a different workflow must be followed <TO BE ADDED>.

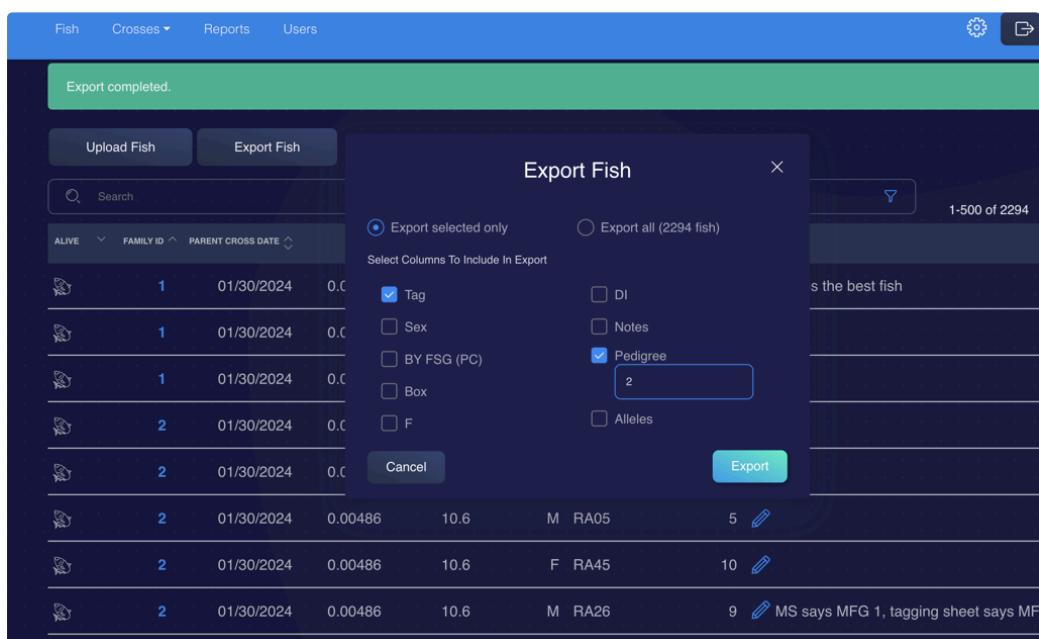
Exporting

If you want to export all the Fish that are currently included in the filter (all the fish currently shown in the table), click on the “Export Fish” button.

If you only want to export a subset of the fish currently showing in the table select by highlighting some part of all the rows you want to include. Then click “Export Fish”.

In the Export Fish dialog that pops up, select the columns you want to export. If you want to export the pedigree. You also need to specify the number of generations you want to include in the pedigree. E.g. If you say 1, the current fish as well as its parents will be included in the exported pedigree. If you say 2, the current fish, its parents and its grandparents will be included in the exported pedigree.

In the example below, only the selected (by highlighting) rows will be included and each Fish's Tag and Pedigree will be included in the output. The pedigree will include 2 generations of ancestors.



Pedigree Output

The pedigree output for a fish is included in a single column with the following format:

<generation ID of fish> (Tag:<tag of fish> CrossDate:<Date parents of fish were crossed> Box:<Box of fish>) ←<generation number> – <generation ID of fish parent 1> (Tag:<tag of fish parent 1> CrossDate:<Date parents of fish parent 1 were crossed> Box:<Box of fish parent 1>) || <generation ID of fish parent 2> (Tag:<tag of fish parent 2> CrossDate:<Date parents of fish parent 2 were crossed> Box:<Box of fish parent 2>) ←<generation number> – <generation ID of ancestor>... etc.

Example of pedigree column value when exporting fish RA76:

193442 (Tag:RA76 CrossDate:2024-01-30 Box:14) ←1-- 180011 (Tag:YA33 CrossDate:2023 Box:6) || 180012 (Tag:OA09 CrossDate:2023 Box:6) ←2-- 170031 (CrossDate:2022) || 170032 (CrossDate:2022) || 171841 (CrossDate:2022) || 171842 (CrossDate:2022)

If any of the data is unknown (e.g. tag or box number) it is left out. If the full cross date is known it is included. Otherwise, only the cross year is shown.

Recommend Crosses Workflow

The **Recommend Crosses** page helps identify optimal crosses for maintaining a refuge population with minimal inbreeding. Users begin by specifying which fish are available for breeding. A table of possible crosses is then displayed, sorted so the *best* crosses appear first, based on the algorithm described in the [Recommended Crosses Design](#) . Users can select crosses for both refuge and supplementation populations. Recommended crosses can be **exported** to a CSV file, or the team performing the crosses can view them directly in the application. Completed crosses can be marked individually in the UI or **imported in bulk** from a CSV file through the [Completed Crosses Page](#) .

Workflow

1. Set available fish

- Users specify which fish are available for breeding.
- Fish must already exist in the system (see [Fish Page](#))

2. View possible crosses

- A table of possible crosses is displayed.
- Crosses are sorted so the *best* crosses appear first, as defined in the [Cross Selection](#) design.

3. Select crosses

- Users select crosses to recommend for the refuge population.
- Crosses can also be selected for a supplementation population.

4. Communicate recommendations

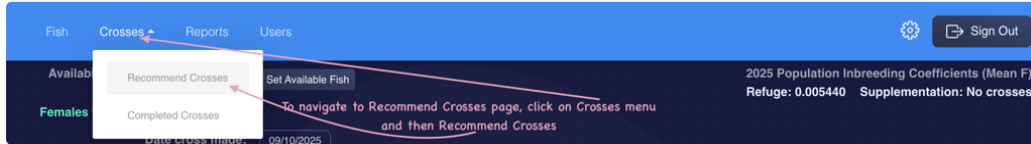
- Recommended crosses can be exported to a CSV.
- Alternatively, the team performing the crosses can log into the application directly.

5. Record completed crosses

- Completed crosses can be marked individually in the UI.
- Crosses can also be batch-uploaded via file (see [Completed Crosses Page](#))

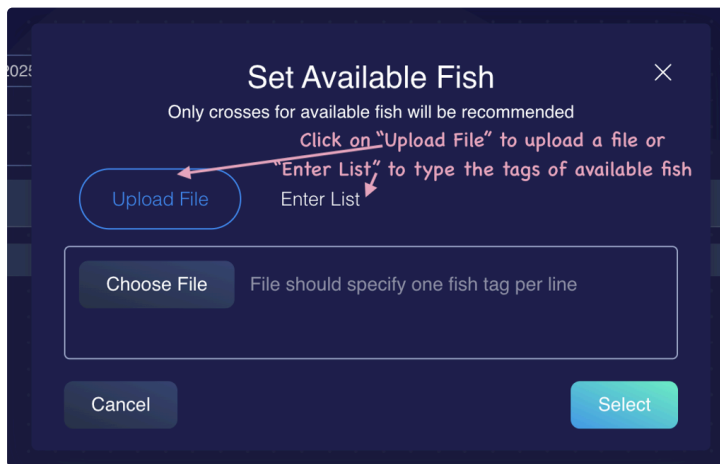
UI

Navigating to Recommend Crosses

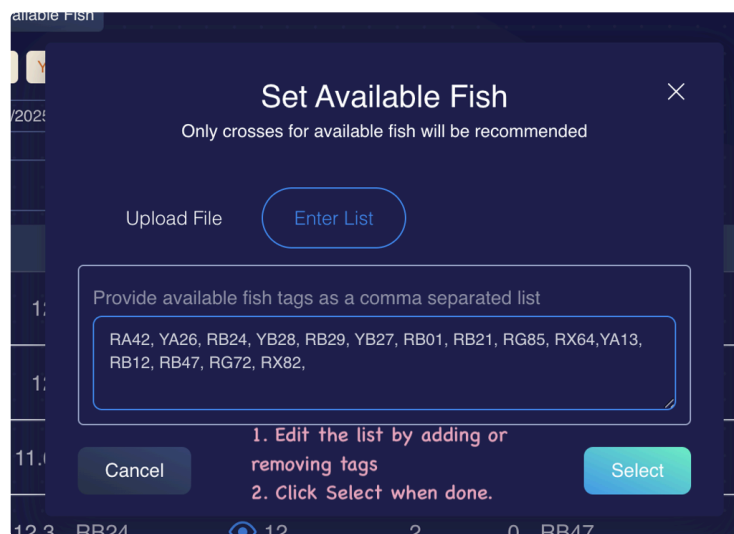


Setting Available Fish

- Click **Set Available Fish** to open the dialog.



- Fish tags may be:
 - Uploaded from a file (one tag per line), or
 - Entered manually.
- After upload, tags can be edited in the **Enter List** workflow.



Selecting Refuge and Supplementation Crosses

Available female fish for crossing: RA42, YA26, RB24, YB28, RB29, (RB01, YB27), RB21, RG85, RX04

All available female fish are shown in blue. This list can be changed by clicking on Set Available Fish. Fish that belong to the same family will be in the same block. Females with 0 or 1 selected males: RA42, YA26, RB24, YB28, RB29, (RB01, YB27), RB21, RG85, RX04

Enter text in the search bar to filter the table for matches on that specific text

Date cross made: 09/10/2025

Click on the filter icon to filter the table on specific properties

1-45 of 45

Export Selected Crosses

The table can be sorted by columns that have chevrons in the header

Select a cross by checking either Refuge or Supplementation. Marking a cross as selected will affect the other crosses that can be selected.

2025 Population Inbreeding Coefficients (Mean F)
Refuge: 0.005440 Supplementation: No crosses
Females that are not yet part of a selected cross are shown in orange. When a tag is selected for a Refuge or Supplementation cross, the tag will be removed from this list.

DATE CROSS MADE	F	DI	F FISH	F PCFSG	M FISH	M PCFSG
02/04/2025	0.00524	11.6	YL23	90	RA10	8
02/11/2025	0.0047	11.5	YA26	8	RC47	22

REFUGE CROSSES COMPLETED WITH FAMILY SIBLING GROUP 8 OF YEAR 2024

DATE CROSS MADE	F	DI	F FISH	F PCFSG	M FISH	M PCFSG
02/04/2025	0.00524	11.6	YL23	90	RA10	8
02/11/2025	0.0047	11.5	YA26	8	RC47	22

REFUGE CROSSES COMPLETED WITH FAMILY SIBLING GROUP 14 OF YEAR 2024

DATE CROSS MADE	F	DI	F FISH	F PCFSG	M FISH	M PCFSG
02/28/2025	0.00501	11.6	RG33	55	RB47	14

No supplementation crosses have been completed with either group 8 of year 2024 or group 14 of year 2024.

In order to see the crosses that have already been completed or requested for a given family, click on the eyeball next to the family ID. Clicking the eyeball again, will close the cross details.

- The crosses table is initially sorted by:
 - Inbreeding coefficient (**f**)
 - Number of crosses already made for each family
- Selected crosses are automatically sorted to the top of the table.
- Users may change sort order (columns and ascending/descending).
- To assist selection:
 - A list of available females that have not yet been crossed is displayed at the top of the page.
 - Clicking the **eye icon** next to a family ID opens details showing all crosses already made with that family.
 - Current **population f values** (for both refuge and supplementation) are shown in the upper-right corner. These values update dynamically as crosses are selected.

Exporting Selected Crosses

- After selection, click **Export Selected Crosses** to download a CSV.
- The file contains two lists (refuge and supplementation), each including:
 - Female tags
 - Female family
 - Male tags
 - Male family
 - f (inbreeding coefficient)
 - Crosses completed for the female's family
 - Crosses completed for the male's family

Completing Crosses

- To mark a cross as completed:
 - a. Set the **completion date** above the table.
 - b. Check **Cross Completed** for each relevant cross.
- Alternatively, upload a file of completed crosses through the [📄 Completed Crosses Page](#)

Completed Crosses Page

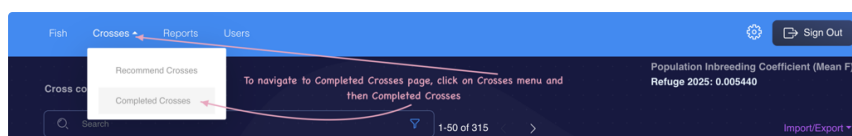
The **Completed Crosses** page provides access to all completed crosses for both refuge and supplementation populations. Populations can be viewed by **year** and **population type**. The page displays the population inbreeding coefficient (Mean F) along with a table of all completed crosses, regardless of whether offspring resulted.

The table includes controls for **searching, filtering, and sorting**, and dropdown menus allow users to switch between year and population type. Completed crosses can be **imported in bulk** from a CSV file. Data can also be **exported** in two formats:

- **Pair cross export** – one cross per line, with both parents shown.
- **Parentage export** – one parent per line (two lines per cross), with allele data and family IDs for both the parent and its offspring.

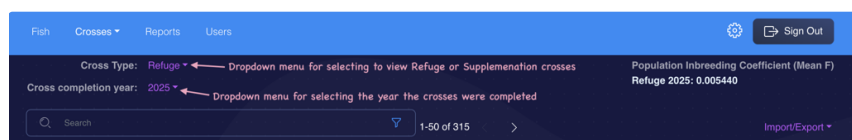
UI

Navigating to Completed Crosses



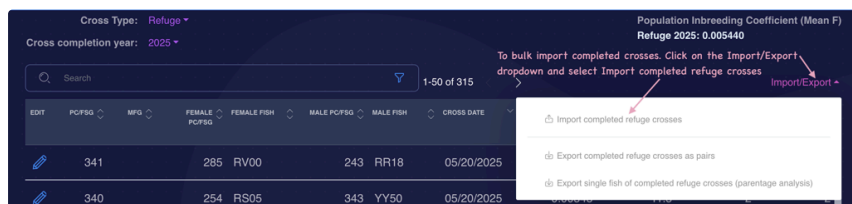
Viewing by Population and Year

Users can choose which population type (refuge or supplementation) and which cross year to view using the dropdown menus at the top of the page.



Importing Completed Crosses

To bulk import completed crosses, open the **Import/Export** dropdown and select **Import Completed <Refuge/Supplementation> Crosses**. The population type of the import is determined by the current view (refuge or supplementation).



The import file must be a CSV with the following required columns:

- Date
- Male

- Female
- <any text>BY<any text>FSG<any text>

A **Comment** column may also be included. If present, values in this column will be added as a **Note** on the completed cross. Columns may appear in any order, but a **header row is required**. Other columns may be included but will be ignored.

Viewing Completed Crosses

By default, the table shows all completed crosses for the selected year and population type. The table can be **sorted, filtered, and searched** (see figure below).

- **Free text search** matches rows containing any of the entered text.
- **Filters** require exact matches. For example:
 - If *Female Fish Tag* is set to **RV**, no results will appear.
 - If set to **RV44**, the table will display the cross where the female parent is **RV44**.

Free text search will filter to rows matching the given text

Table can be sorted by clicking on chevrons in column headers

Click on pencil to edit cross

Click the filter icon to filter the table by specific properties

EDIT	PC/FSG	MFG	FEMALE PC/FSG	FEMALE FISH	MALE PC/FSG	MALE FISH	CROSS DATE	F	DI	FEMALE PC/FSG CROSSSES COMPLETED	MALE PC/FSG CROSSSES COMPLETED
	341	285	RV00		243	RR18	05/20/2025	0.00464	11.3	2	2
	340	254	RS05		343	YY50	05/20/2025	0.00545	11.5	2	2
	348	171	YX73		300	RX18	05/20/2025	0.00478	11.2	4	2

When clicking the filter icon, the filter dialog appears (see figure below).

Search

PC/FSG:

MFG:

Female PC/FSG:

Female Fish Tag:

Male PC/FSG:

Male Fish Tag:

Close Search

Editing Completed Crosses

To edit a cross, click the **pencil icon** in the row. This opens a panel below the row with editable fields.

- Click the pencil again to close the panel.

Free text search will filter to rows matching the given text

Table can be sorted by clicking on chevrons in column headers

Click on pencil to edit cross

Click the filter icon to filter the table by specific properties

EDIT	PC/FSG	MFG	FEMALE PC/FSG	FEMALE FISH	MALE PC/FSG	MALE FISH	CROSS DATE	F	DI	FEMALE PC/FSG CROSSSES COMPLETED	MALE PC/FSG CROSSSES COMPLETED
	348	174	YX73		300	RX18	05/20/2025	0.00478	11.2	8	4
	345	297	RX46		282	RV55	05/20/2025	0.00529	11.5	3	2

MFG can be changed and will be reflected in the row

Notes

Existing notes will be visible in Notes text field and are editable

Existing note

☐ Cross failed
☐ Cross included in supplementation

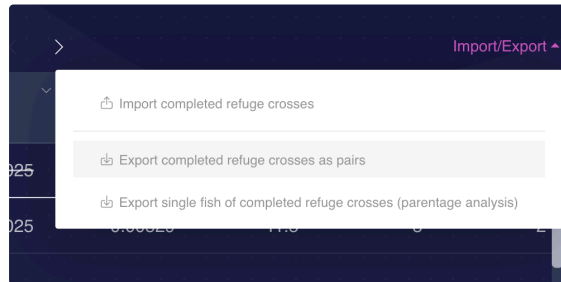
If a cross is included in supplementation, the cross will also be seen in the supplementation view

If a cross is marked as failed, the row will be seen with a strikethrough

Exporting Crosses

From the **Import/Export** dropdown, two export options are available. Both exports include only the crosses currently visible in the table (i.e., filters and searches are applied).

- **Completed <Refuge/Supplementation> Crosses as Pairs** – one cross per line, both parents listed. Details of the cross (e.g. f, DI, etc) are included.
- **Single Fish of Completed <Refuge/Supplementation> Crosses (Parentage Analysis)** – one parent per line, two lines per cross, genetic data for the parent is included.



User Management

To add, remove, or disable users, click **Users** in the top navigation bar.

Adding Users

When a new user is added, their account will be created with the specified username and a default password of **pass**. Upon first login, the user must change their password via the [User Settings](#) page.

User Associations

Every action in the system is tied to a specific user (e.g., adding fish, selecting possible crosses, recording completed crosses, or editing crosses). If a user is deleted, their past actions will remain in the system, but no new actions can be associated with that account—even if a new user is later created with the same username.

Disabling vs. Deleting Users

If you want to prevent a user from logging in but may need to restore access later, it is best to **disable** the user rather than delete them.

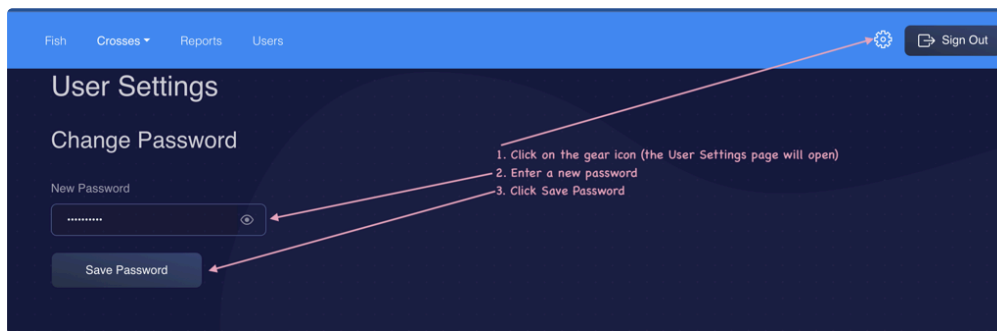


User Settings

Currently, the only available user setting is the **password**.

To change your password:

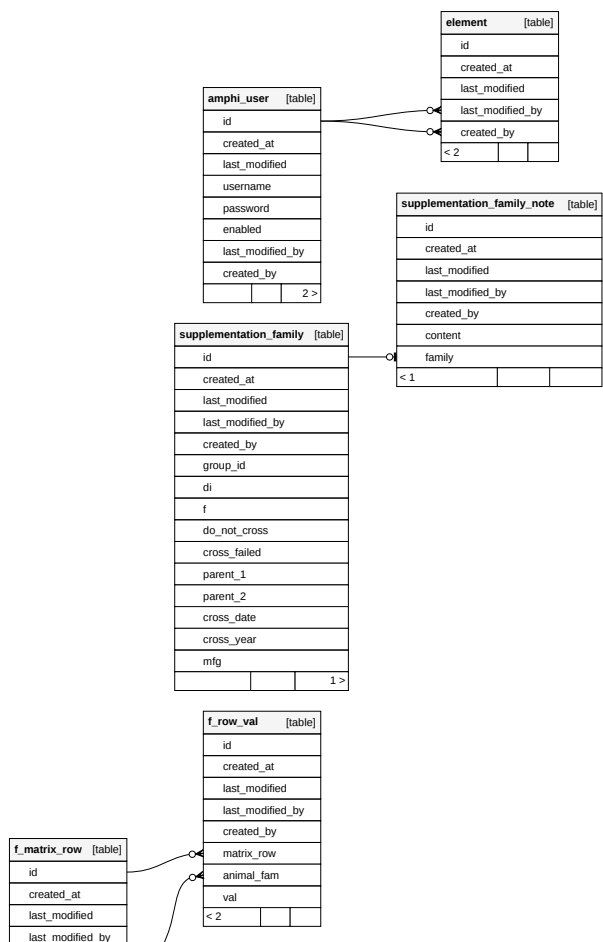
1. Click the **gear icon** in the upper-right corner of the page.
2. Enter your new password.
3. Click **Save Password**.

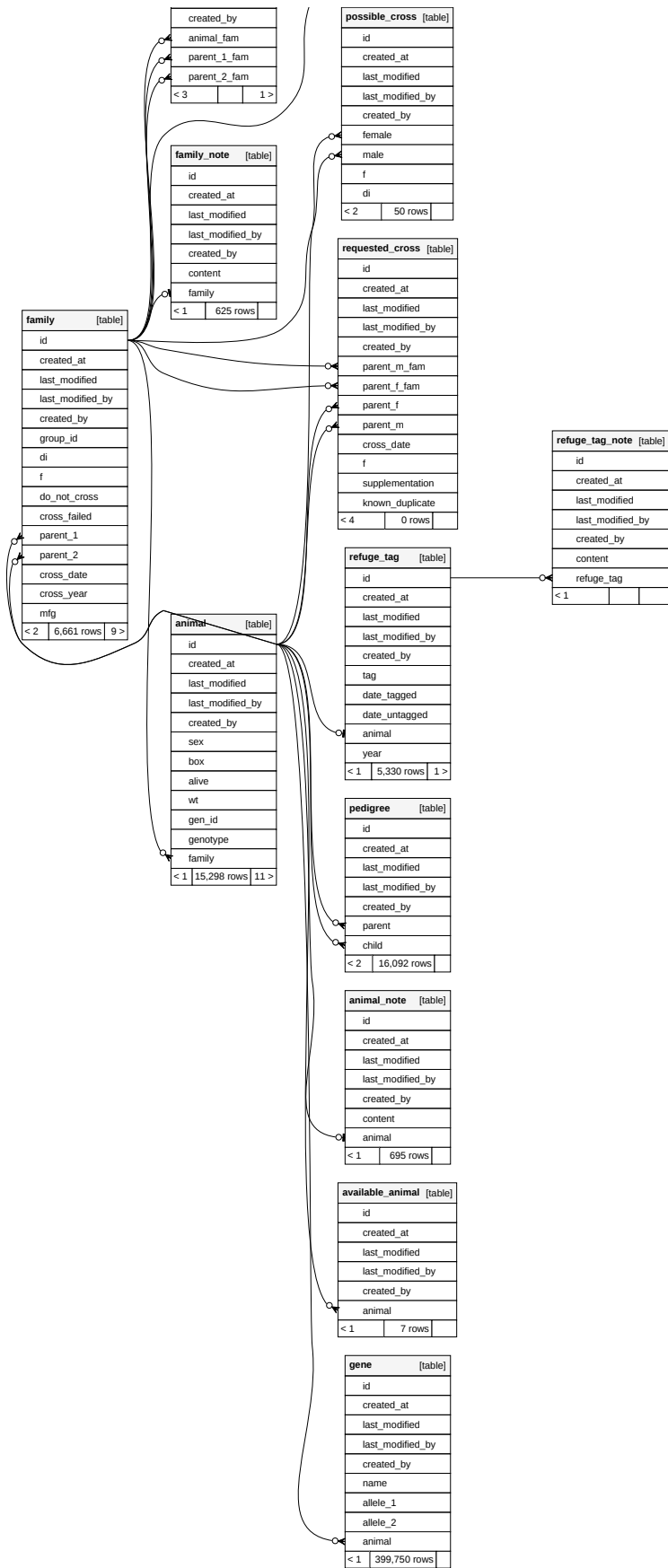


Running Software

Directions for building and running the software can be found in the top-level README of the amphitrite [github respository](#).

Data Model Diagram





Generated by SchemaSpy

Amphitrite Data Model

Cross Selection Algorithm

Given a female fish ID and set of available males supplied by the user

1. Determine family of female fish

Don't do select different crosses for females from the same family. If there is more than one female from the same family then refuge chooses which one to use.

2. Rank by relatedness for all possible crosses:

- a. Relatedness determination from PMx (Lacy et al. 2012), using the inbreeding coefficient f . f is determined for the to-be-born generation. The f value must be below 0.01. Calculation is described here: [Nature Research Lab - Recovery Mode](#)

3. Check need-to-cross numbers. If need-to-cross value for the 2 fish families is $n > 0$, remove the hypothetical cross from need-to-cross before determining the cross.

4. ~~Check domestication index (DI); if DI is above n , do not use that cross.~~ The DI value will be supplied by the user, but the software will not automatically exclude possible crosses based on DI

$$DI_{\text{Offspring}} = (DI_{\text{FemaleParent}} + DI_{\text{MaleParent}})/2 + 1$$

5. Update need-to-cross appropriately as crosses are selected.

F (Inbreeding Coefficient) Calculation

Path Analysis

Previous generations f values calculated using path analysis as described here: [Nature Research Lab - Recovery Mode](#)

Those values were then saved and stored in the git repository:

[amphitrite/amphitrite/src/app/importer/resources/f_values.csv at main · adstruble/amphitrite](#)

The f values are then uploaded during db instantiation along with the existing pedigree and fish and family entities that compose the pedigree. This is done to save time. The implementation of the f value calculation exists within the code base, but to calculate the f values for the entire pedigree (through crosses completed in 2023) took 1 -2 days on an 8 core m1 with that current implementations

Tabular Method

To calculate f values of individuals resulting from potential future crosses, the tabular method will be used instead as it is significantly faster than path analysis and results in very similar (although not identical results)

[🔗 Calculating inbreeding and relationship, the tabular method](#)

Note on the above link: The value added to the 1s in the diagonal is the f value